

Spatial modeling in support of measles control and elimination

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The contribution of models



Program questions

- Where are gaps in routine MCV coverage?
- Where are there unvaccinated persons?
Where are the remaining susceptibles?
- Where is there likelihood of transmission?
- What is the relative importance of doses received via RI and SIAs?
- How can SIA effectiveness be measured?
How do we best plan SIAs?
- How effective is outbreak response vaccination?

Cutts et al. (2020)

But how do we get there?

Program questions



VS

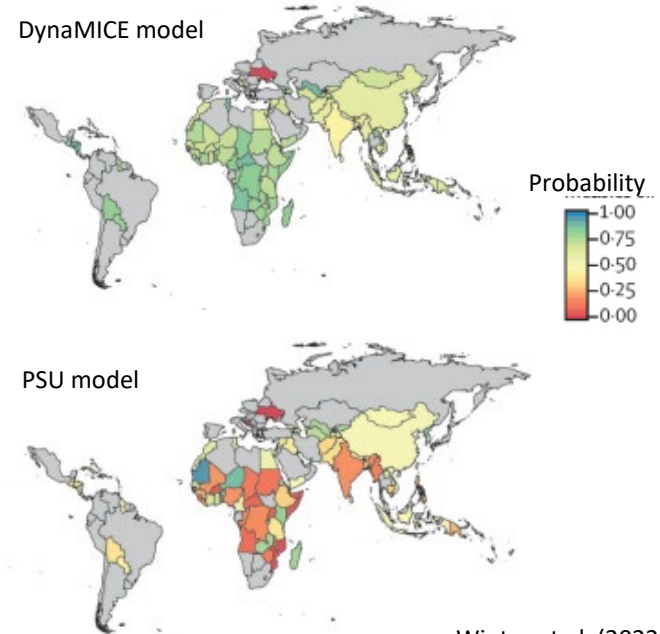
Program benchmark



Existing benchmarking for measles elimination focuses on threshold coverage targets or “snapshot” scenarios

- Vaccine coverage targets*:
95% MCV1 and MCV2 at national or district level
- Surveillance targets*:
≥2 suspected cases per 100 000 population discarded as non-measles and non-rubella
- Regional goals:
6 WHO regions

Probability of measles elimination by 2050 with intensified investments



Historical examples demonstrate that high levels of MCV coverage is neither necessary or sufficient for elimination

Category	Number of Countries	MCV1 >95%	MCV1 <95%
Verified	82	28 (34%)	54 (66%)
Eliminated	21	5 (24%)	16 (76%)
Endemic	85	16 (19%)	69 (81%)
Re-established endemic transmission post-verification	5	2 (40%)	3 (60%)
No report	1	1 (100%)	0 (0%)

Data source: Regional Verification Reports; Crowcroft et al. (2024)

How can modeling provide better performance metrics to drive and assess programmatic decisions?

Outline



- Motivation
- Model and Calibration
- Spatial coverage distributions
- Conclusion

We require high spatial and individual resolution

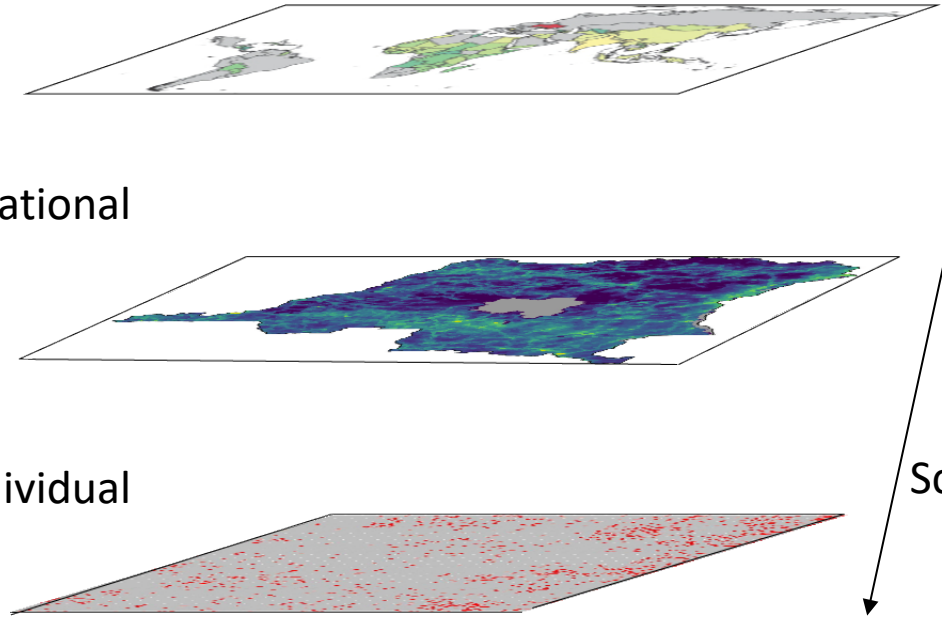
Global, Continental, National

We want to model individual agents on multi-national scales

Subnational

Individual

Scale factor

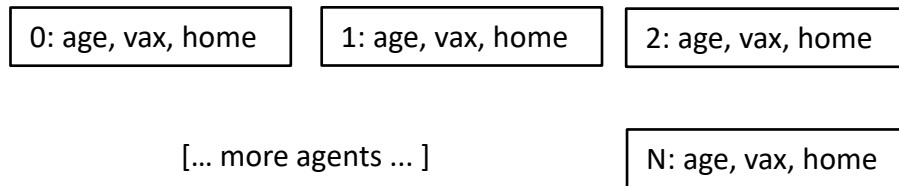


Figures from Winter et al (2022), Cheng et al (2021), and Truelove et al. (2019)

Leveraging software and hardware designs

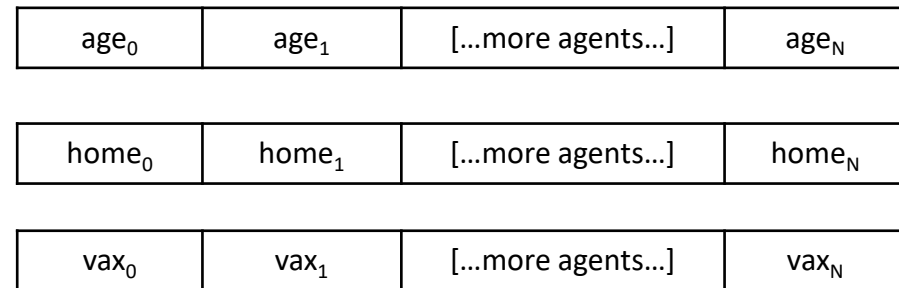
- Properties as arrays
- “Just the properties” philosophy
- Reducing reporting
- Deterministic demographics
- Cohorts(ish)
- New(ish) algorithms
- Interpreted, dynamically types languages (e.g., python) + JIT

agents



VS

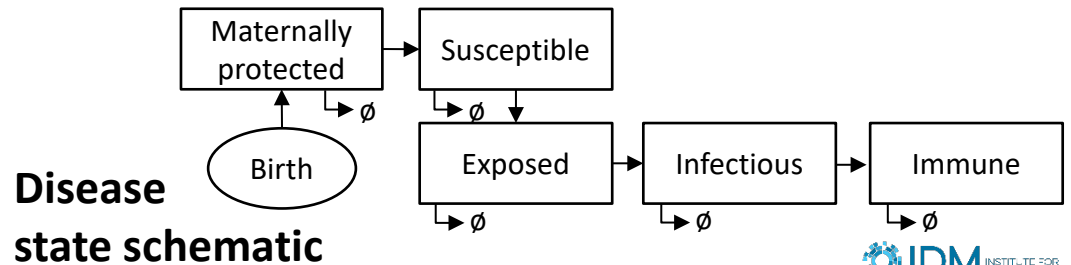
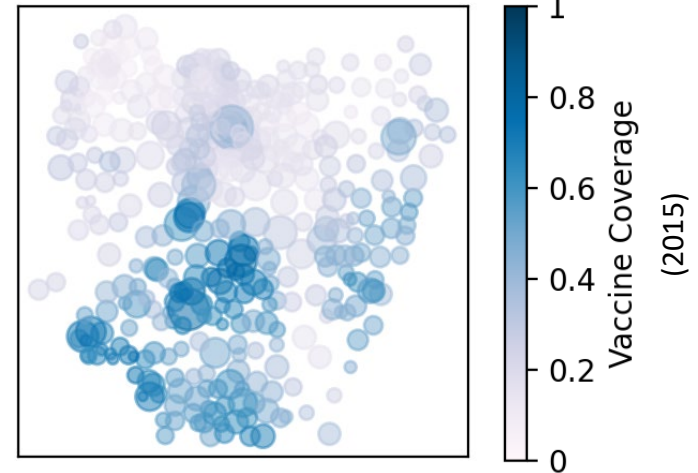
properties



We build a high spatial resolution model using a python framework for agent based spatial disease models (LASER)

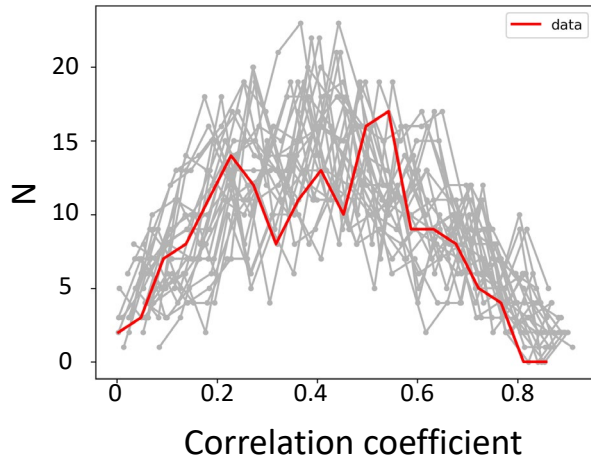
- Northern Nigeria Scenario (Admin 2)
 - Vaccine coverage
 - Demographics (population and vital dynamics)
- Scenario used for calibration
- Agent based, metapopulation model written in python with acceleration via numpy and numba
- 419 nodes, 96M initial agents
- Gravity model

Northern Nigeria Map

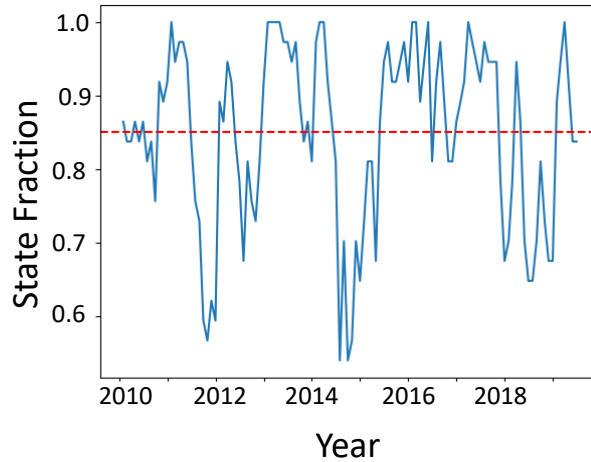


We calibrate against spatio-temporal data from Northern Nigeria spanning 2010 to 2020

Spatial Correlation



Fraction of States with Cases



Potential other data sources for calibration:

- Historical case data
- Seasonality
- Case age distribution
- Serology surveys
- Travel data
- Night lights
- ...

Limitations:

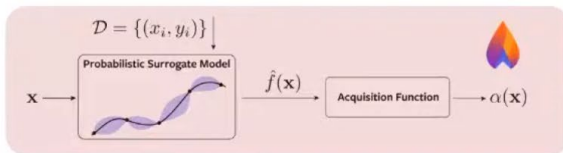
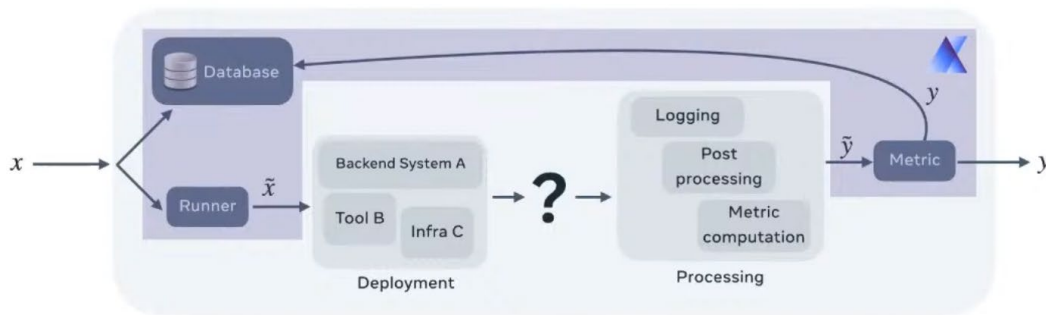
- Under-reporting
- Heteroskedasticity
- Impact of SIAs
- Uncertainty in inputs/initial conditions (e.g., demographics)
- Applicability to future scenarios

We leverage an adaptive experimentation platform to calibrate this noisy, multi-objective problem +

Ax is an accessible, general-purpose platform for understanding, managing, deploying, and automating adaptive experiments.

- Versatile
- Customizable
- Production-complete
- Multi-modality and constraints
- High-noise settings
- Easy to use

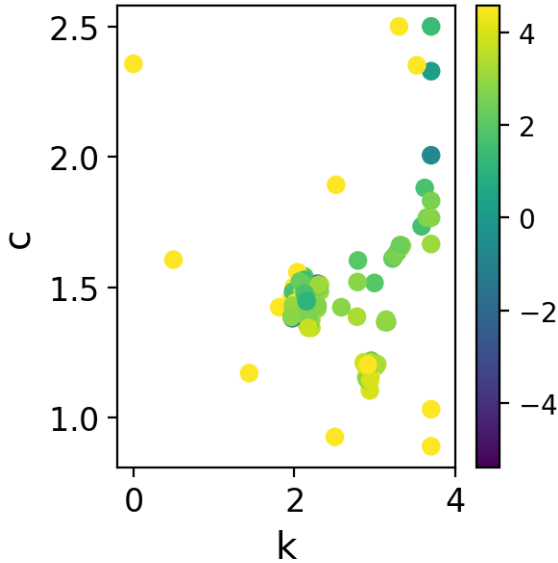
Ax + BoTorch conceptual framework



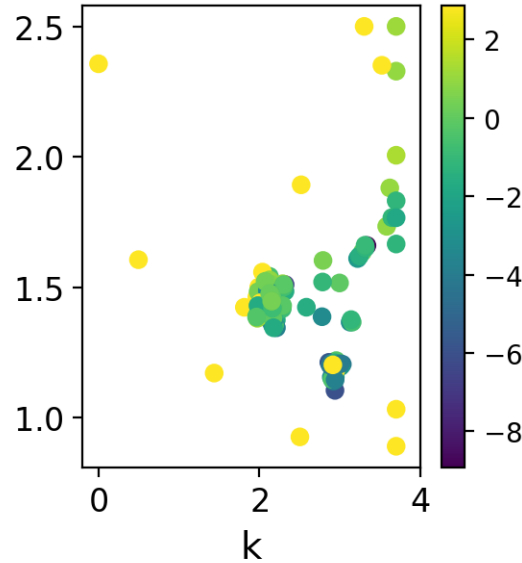
Multi-objective calibration of gravity model parameters

Spatial correlation

mean

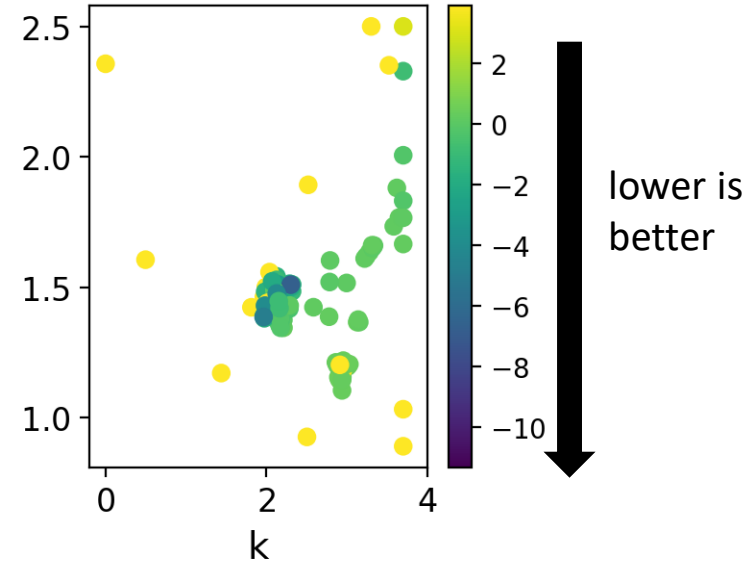


width



Network spread

mean

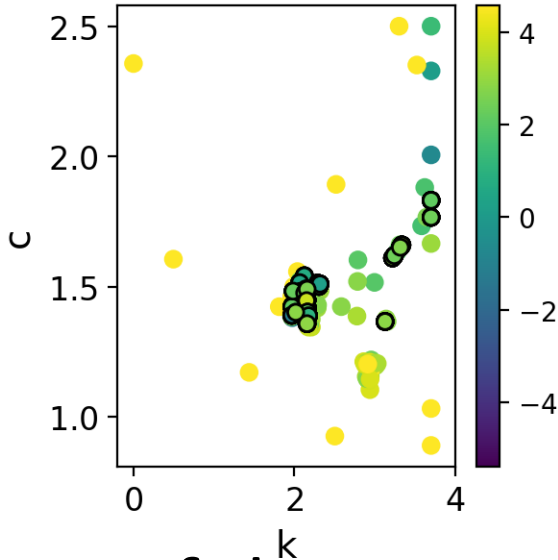


126 samples using the ax+botorch “out of the box”

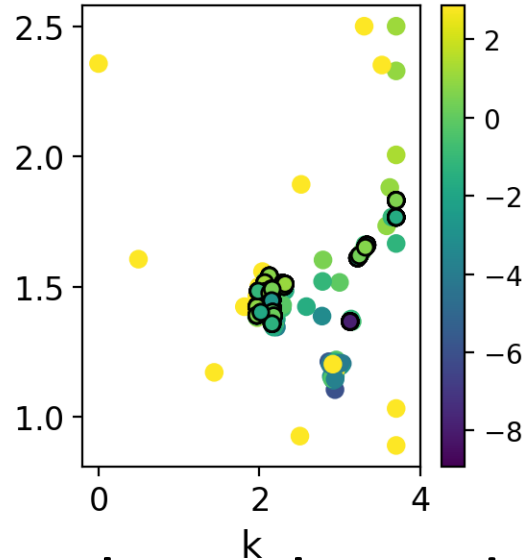
Multi-objective calibration of gravity model parameters define a pareto-front

Spatial correlation

mean

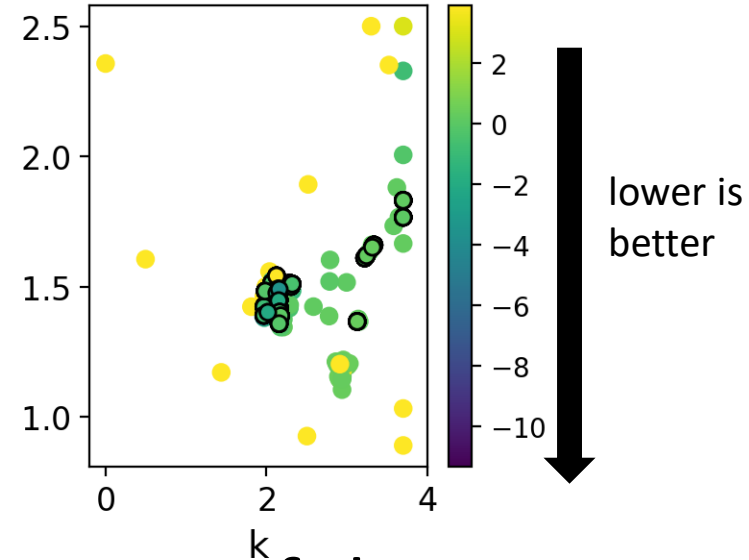


width



Network spread

mean

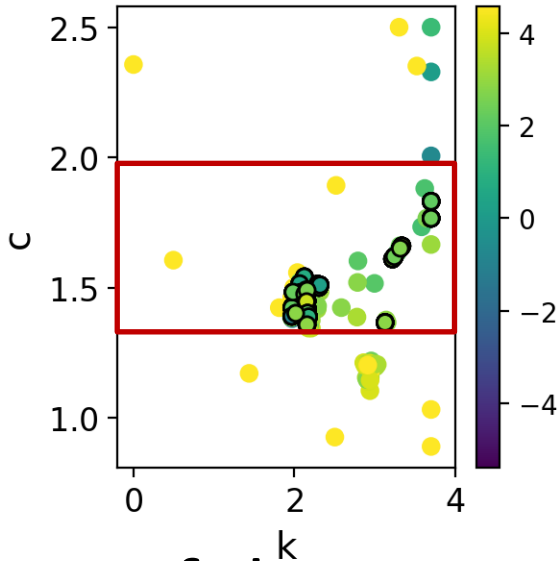


33 of the 126 samples selected as part of the pareto front

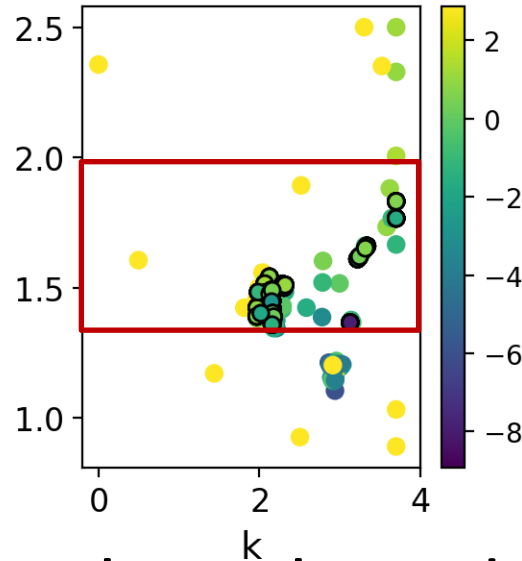
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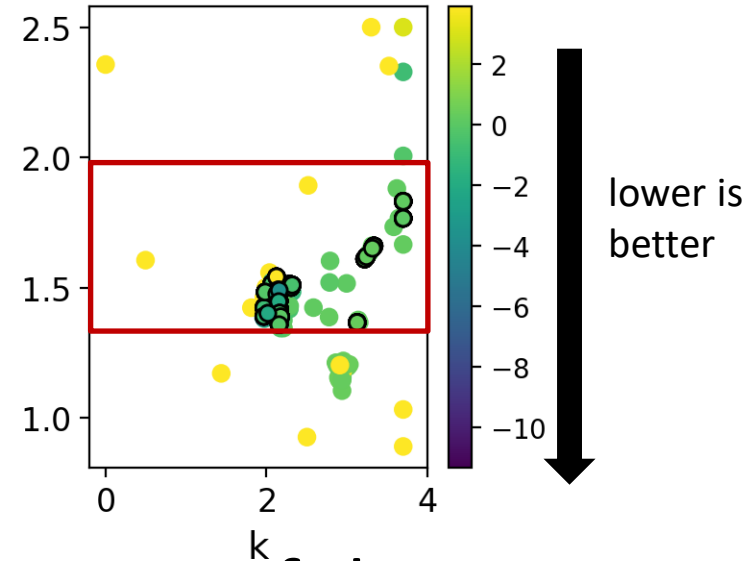


width



Network spread

mean

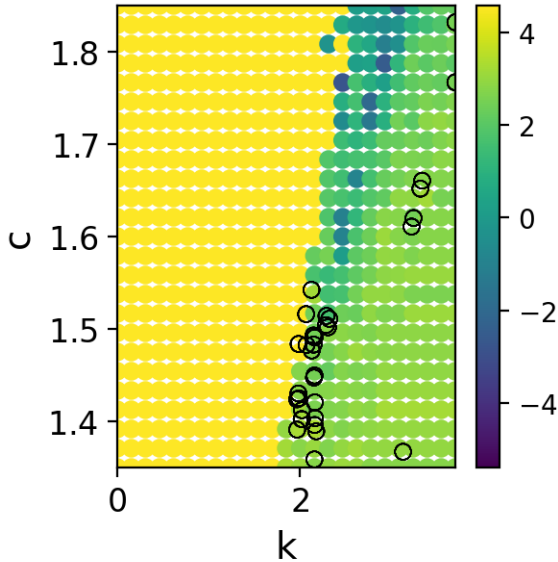


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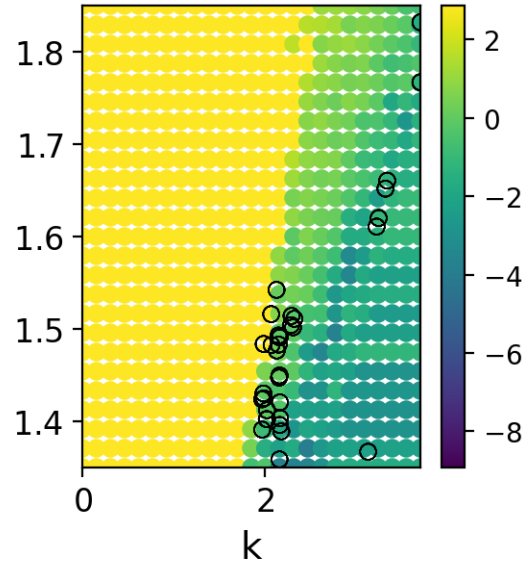
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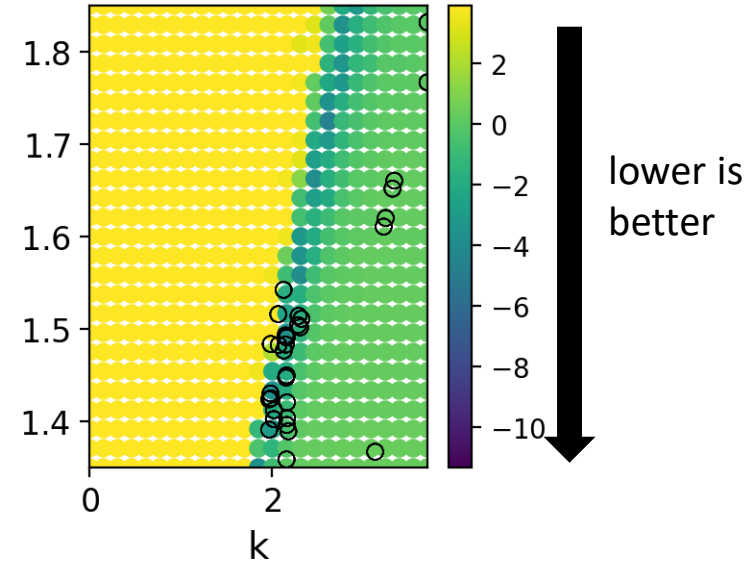


width



Network spread

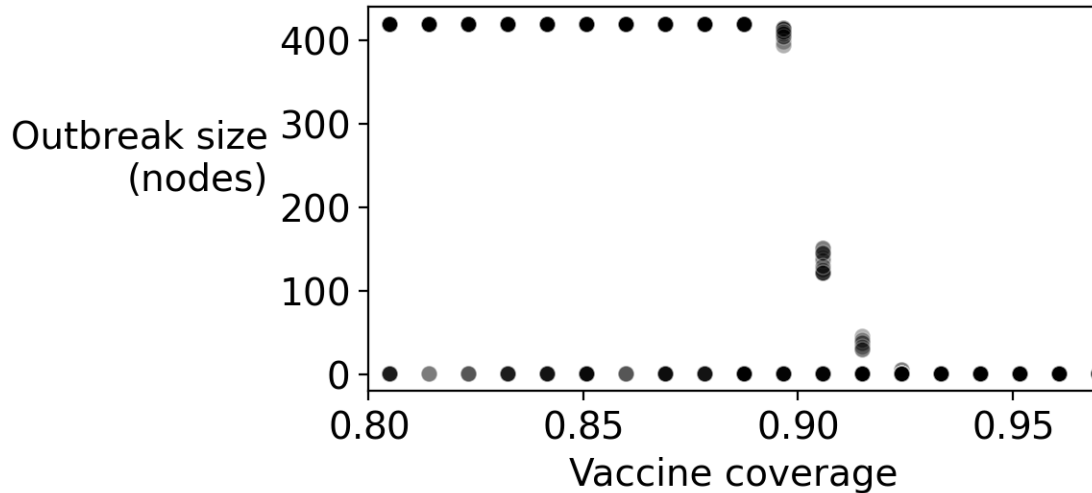
mean



6250 simulation grid search

We look at transmission through the network as a metric of how local outbreaks might threaten elimination status

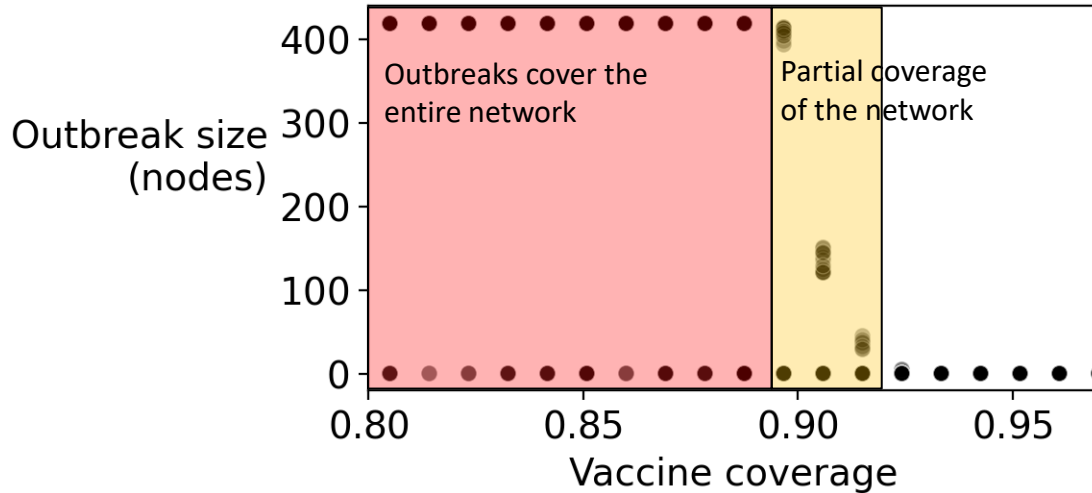
Transmission through the network



- Uniform vaccine coverage ranging from 75% to 97%
- Seed network with a single infected individual
- Plot number of nodes with an outbreak after 4 years
- N = 25 random seed samples per vaccine coverage level

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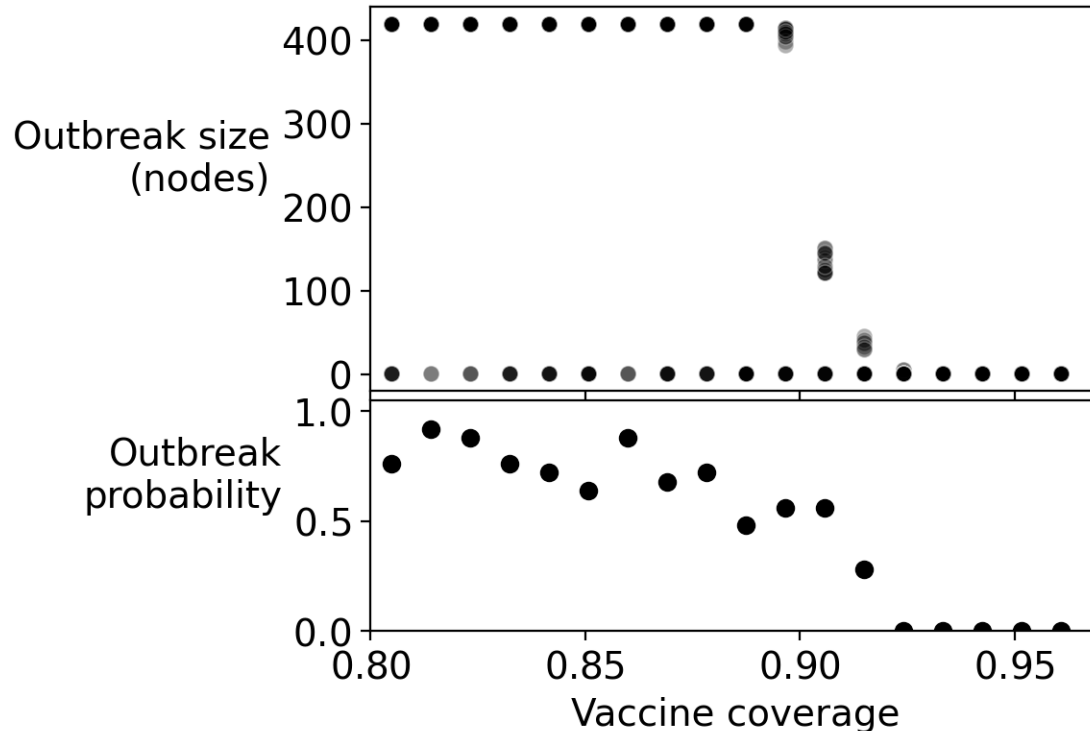
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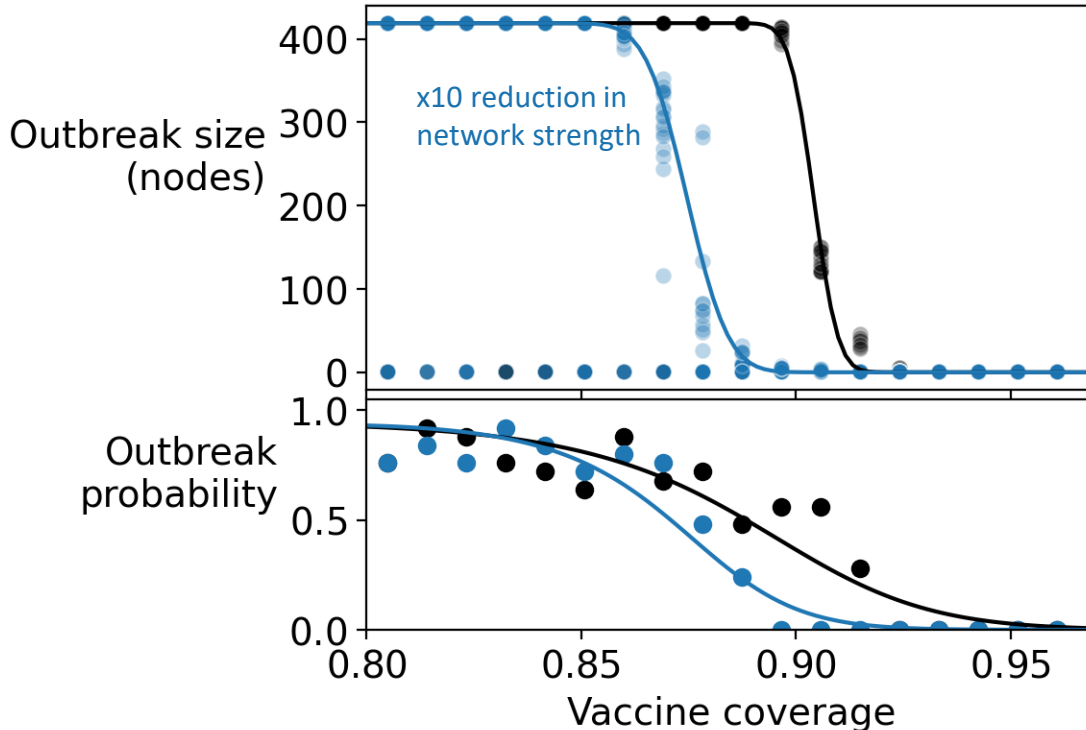
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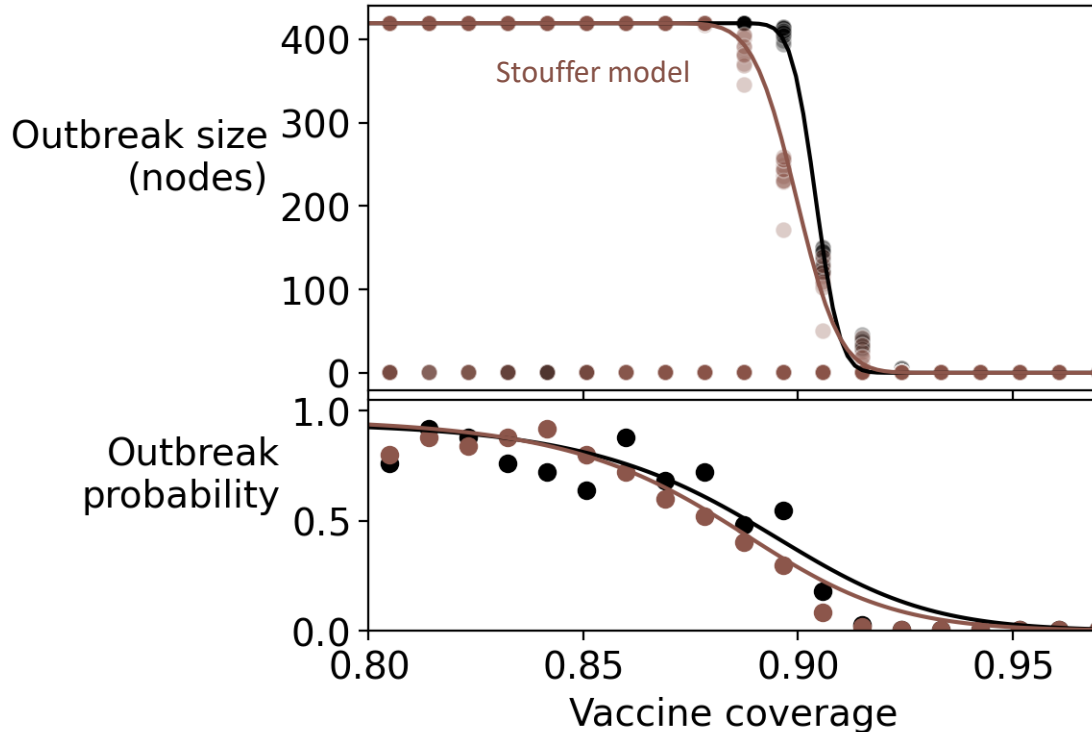
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We are also looking at other spatial network designs

Transmission through the network



- Uniform vaccine coverage ranging from 75% to 97%
- Seed network with a single infected individual
- Plot number of nodes with an outbreak after 4 years
- Compare gravity to Stouffer model: outbreak probability similar, but extent may be different
- How can we motivate our choices?

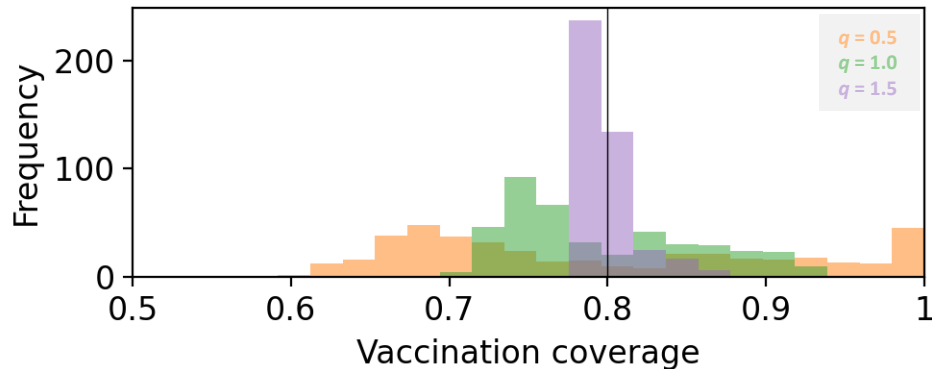
We use existing vaccination maps to build distributions with a target coverage

Scale initial Northern Nigeria node vaccine coverage ($V_i(0)$; below) to total target coverage $V_N(t)$:

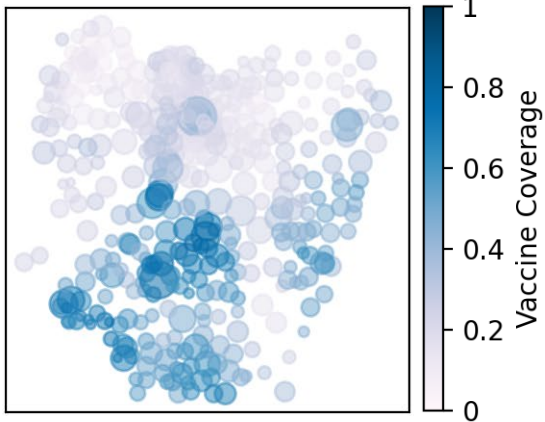
$$V_i(t) = V_i(0) - \left(\frac{V_N(0) - V_N(t)}{\sum_{j=0}^N p_j V_j^q(0)} \right) V_i^q(0)$$

q is our equity factor where increasing q corresponds to increasing equity.

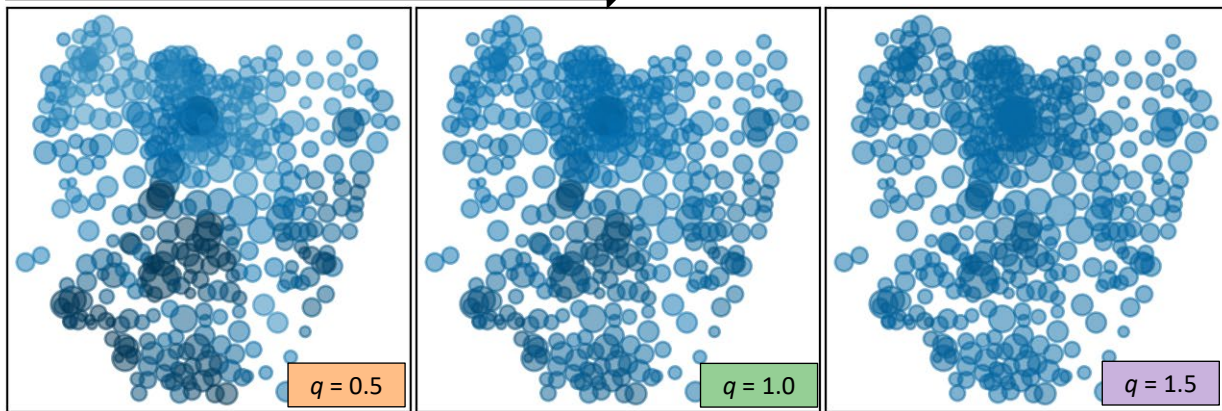
Winter et al. (2022)



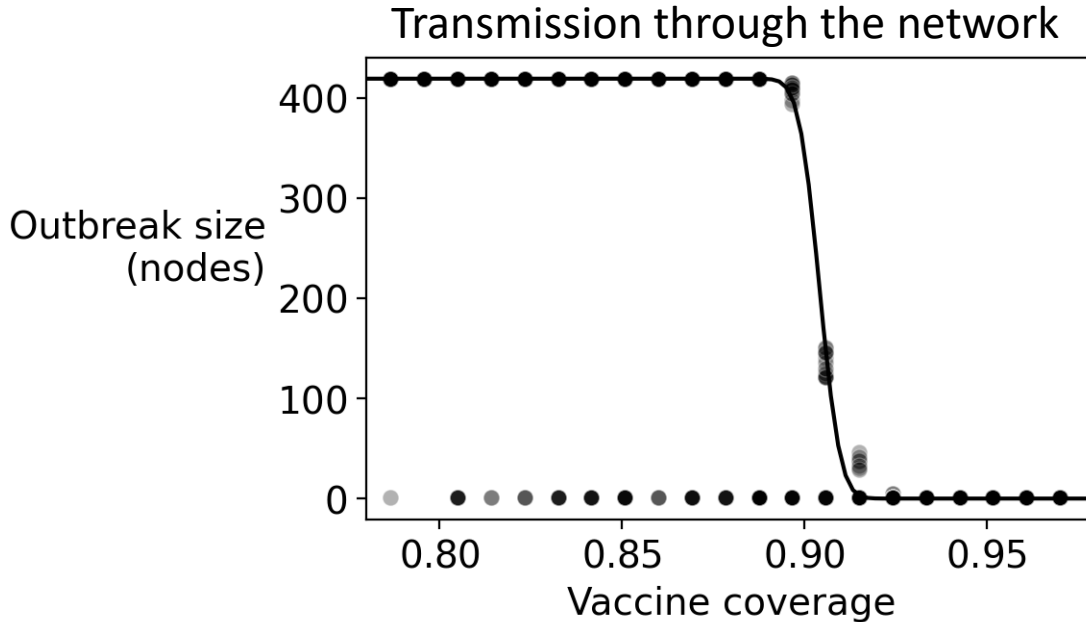
Original coverage



Increasing q , increasing equity



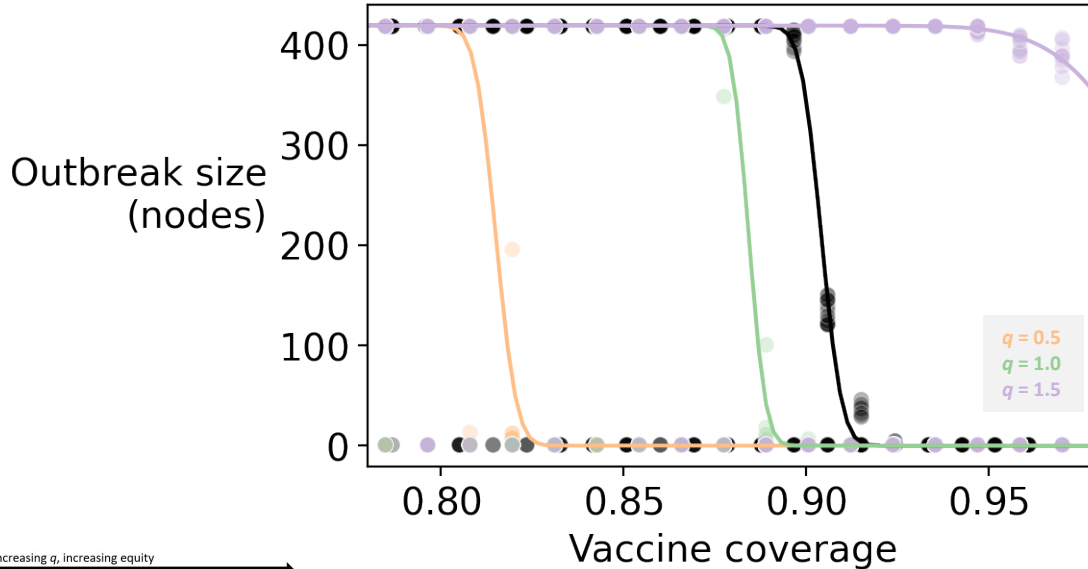
We construct “pattern based” vaccine coverage distributions to investigate impact of vaccine equity



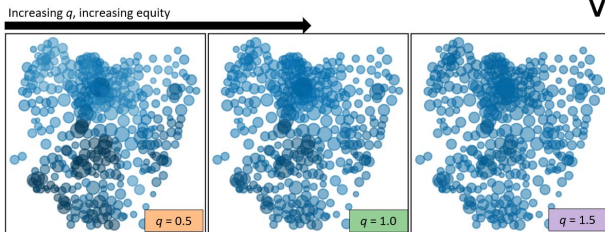
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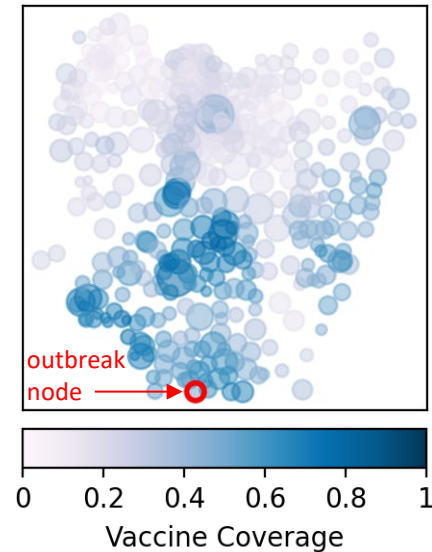


- Uniform vaccine coverage ranging from 75% to 97%
- Seed network with a single infected individual
- Plot number of nodes with an outbreak after 4 years
- $N = 25$ random seed samples per vaccine coverage level
- Introducing spatial structure to RI coverage sees fewer outbreaks in least equitable scenario – why?



A closer look at the importation and distribution conditions highlights their importance

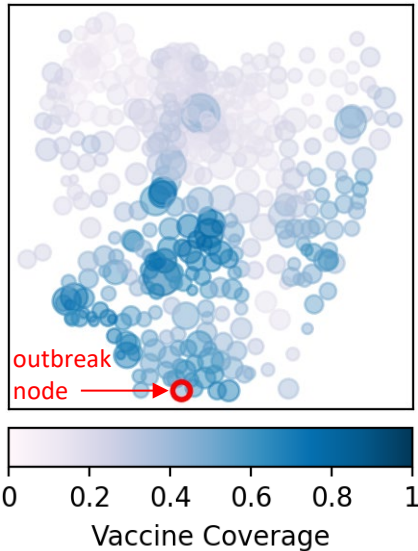
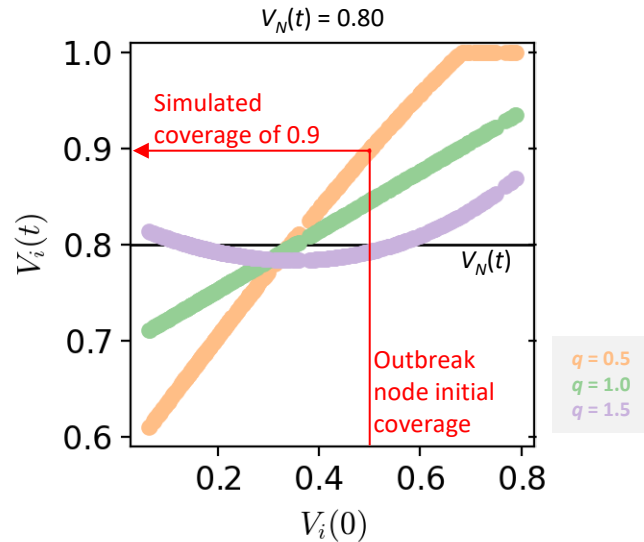
- Seeding in single node with relatively high initial coverage means that low q favors that node



A closer look at the importation and distribution conditions highlights their importance

Parameterized coverage versus input (data) coverage

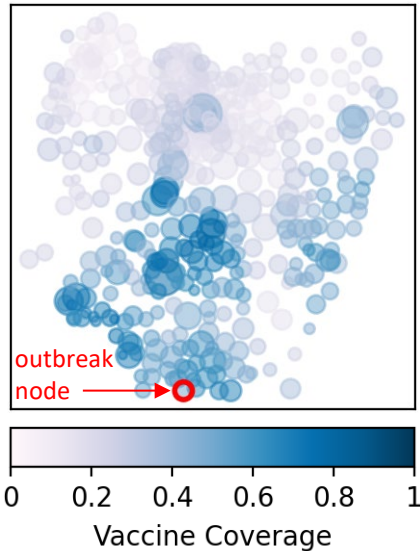
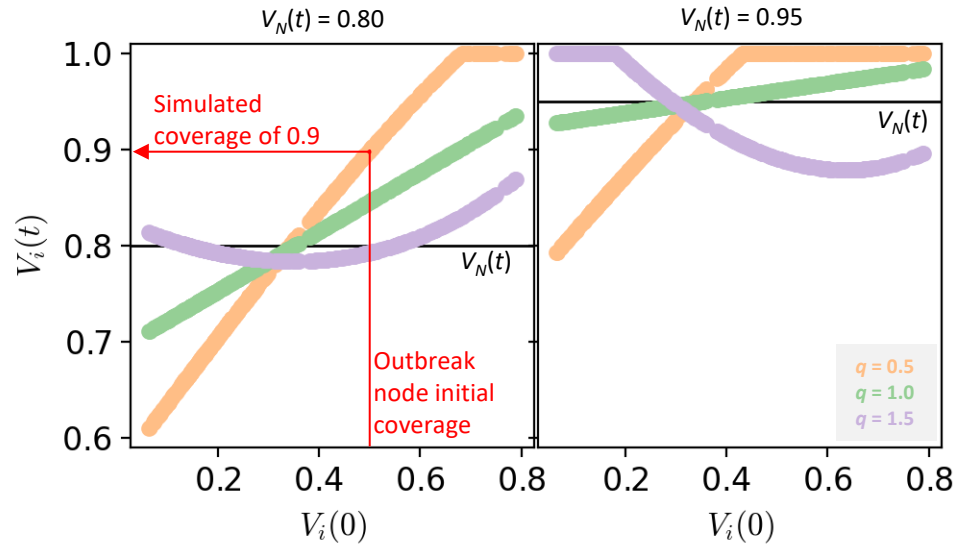
- Seeding in single node with relatively high initial coverage means that low q favors that node
- Coverage parameterization leaves many nodes below target $V_N(t)$ for high q
- What are alternative importation schemes?



A closer look at the importation and distribution conditions highlights their importance

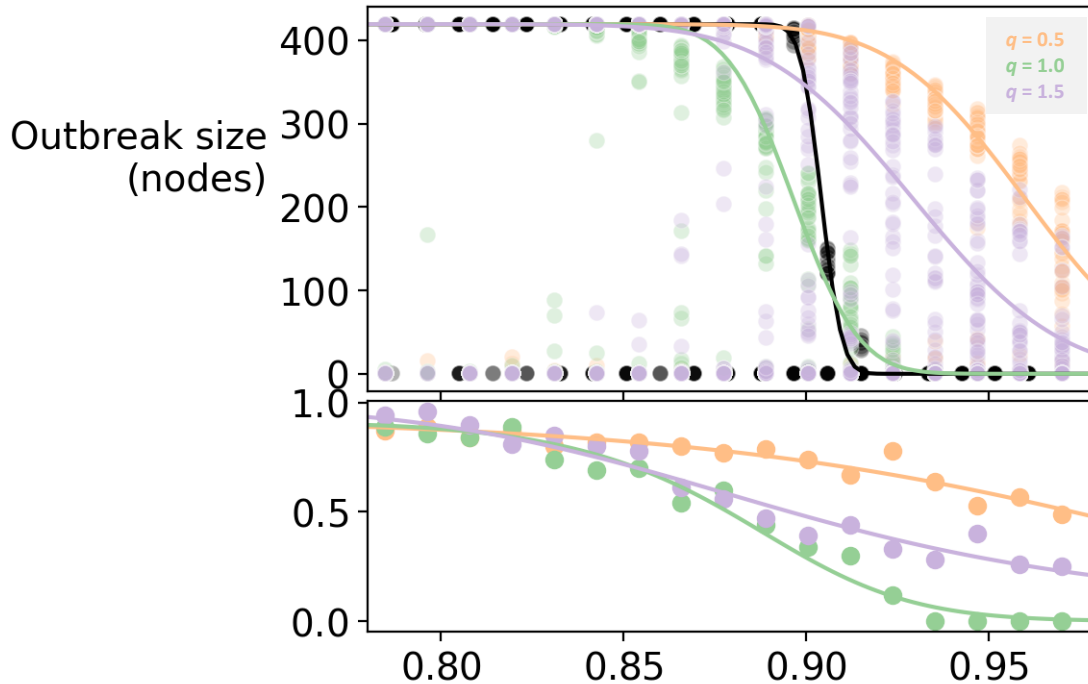
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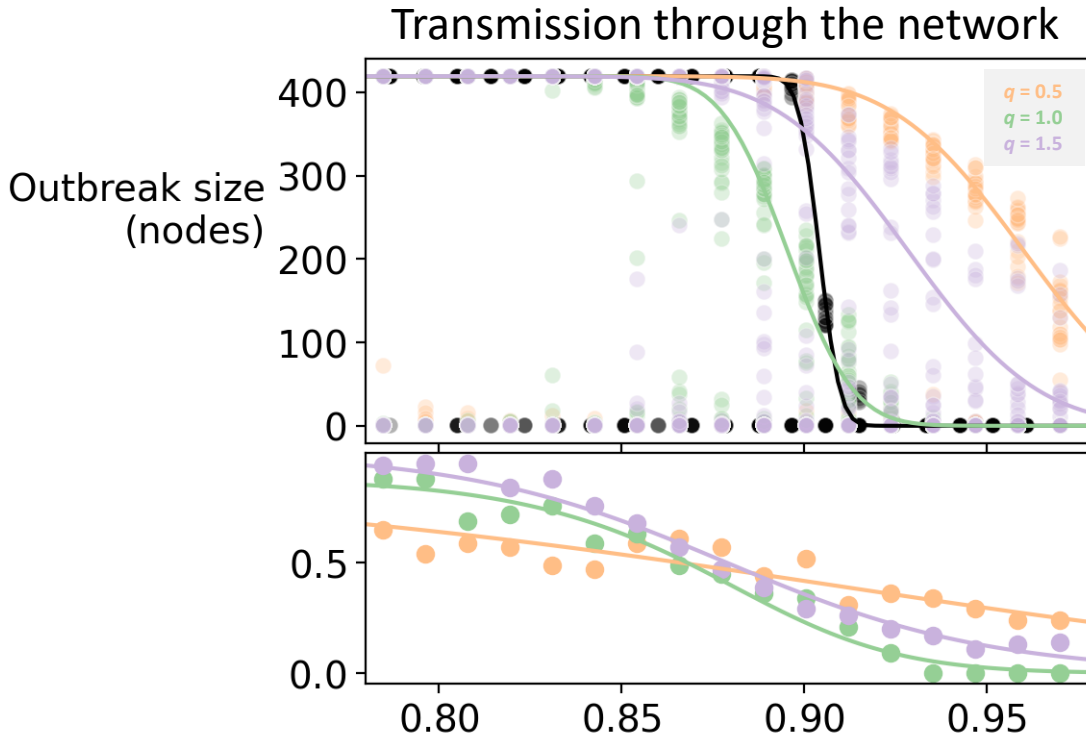
Weight importation event by zero dose population now has least equitable scenario trending towards outbreaks

Transmission through the network



- Uniform vaccine coverage ranging from 75% to 97%
- Seed network with a single infected individual
- Plot number of nodes with an outbreak after 4 years
- $N = 100$ random seed samples per vaccine coverage level

Weight importation event by population is quite similar to zero dose scenario



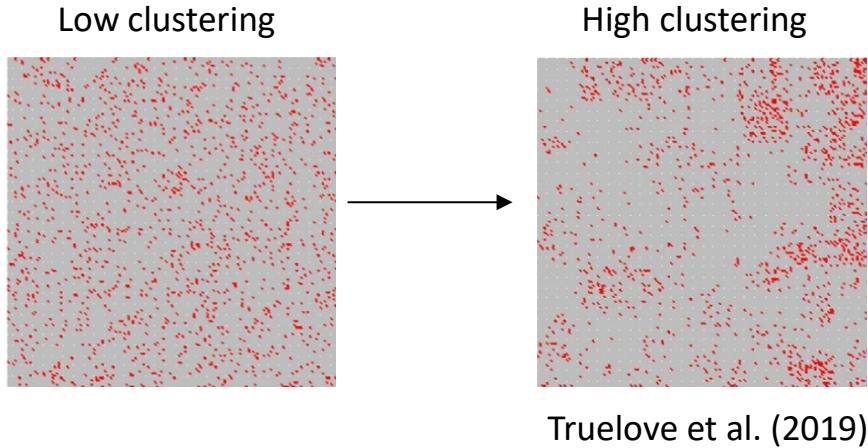
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Conclusion

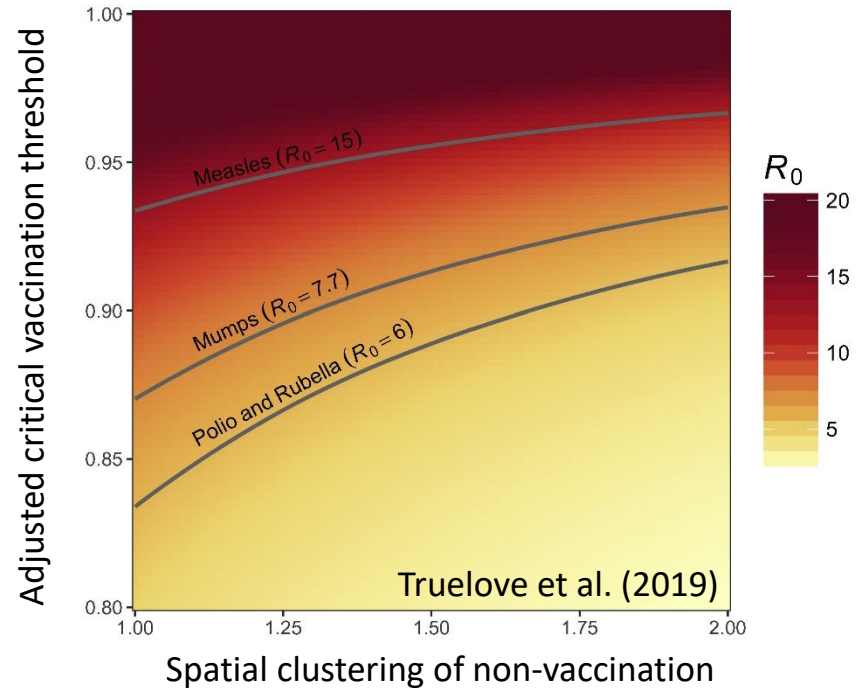
- Clear need for new tools and thinking towards measles elimination
- Opportunity for additional benchmarking
- Thinking beyond national and subnational coverage:
 - Connectivity/network models
 - Importation risk
 - Equity and coverage patterns
- Opportunity areas:
 - Inputs and projects for initial conditions (e.g., demographics, connectivity, mobility models)
 - Model calibration and validation

Spatial clustering of non-vaccinated individuals can increase required vaccination rates to avoid large outbreak

Visualization of spatial clustering of non-vaccinated individuals

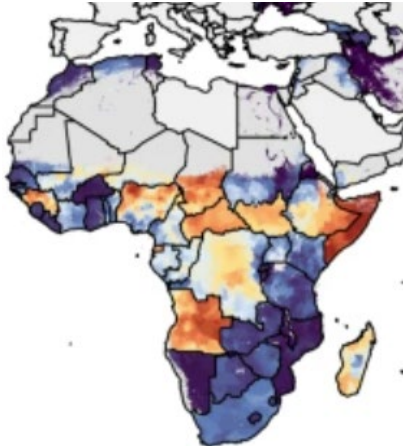


Impact of spatial clustering on vaccination coverage necessary to avoid outbreaks

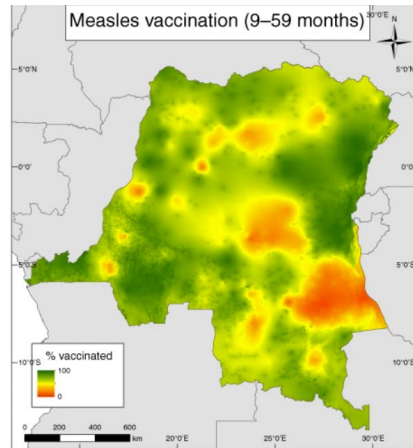


How can we create spatial distributions of vaccination coverage for our simulations?

MCV Vaccination

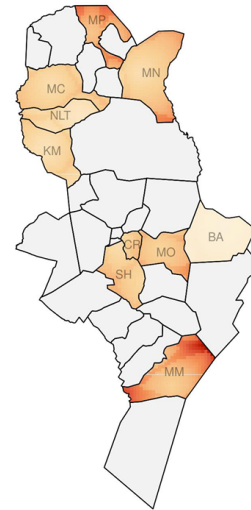


Sbarra et al. (2020)

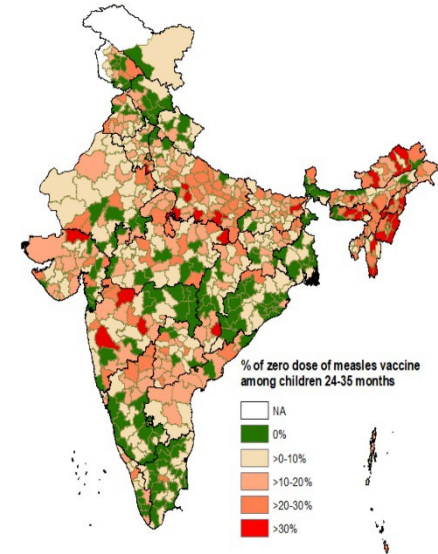


Utazi et al (2019)

Zero dose (MCV)



Arambepola et al. (2021)



Dhalaria et al. (2024)

References

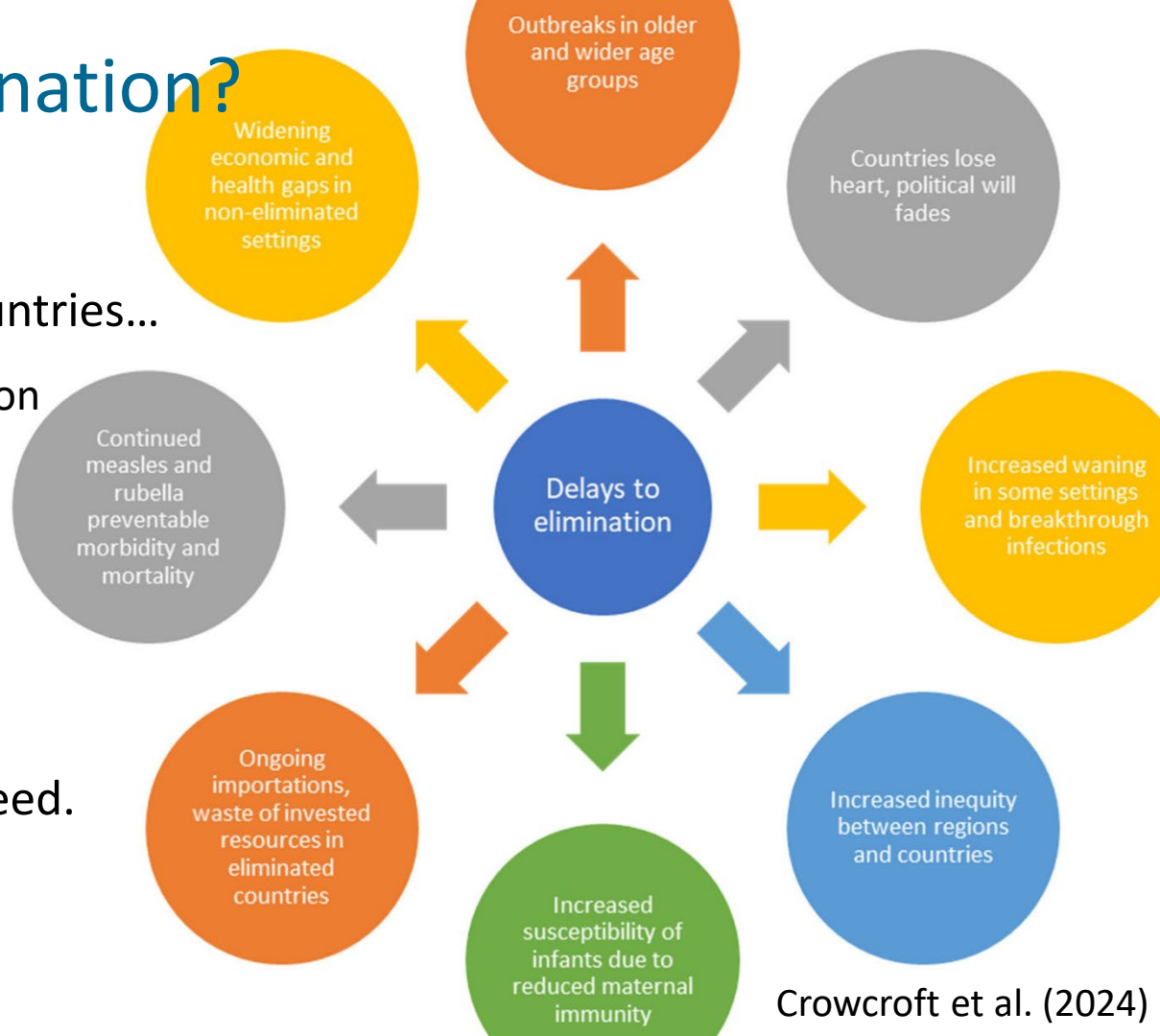
- [Accelerating measles elimination in the Western Pacific Region during the calm between the storms](#)

Why measles elimination? Why now?

Delay elimination in some countries...

- Increasing inequity in vaccination coverage means outbreaks are more likely and larger
- Difficult to sustain political will
- Waning immunity may re-establish transmission

makes it harder for all to succeed.



We require high spatial and individual resolution

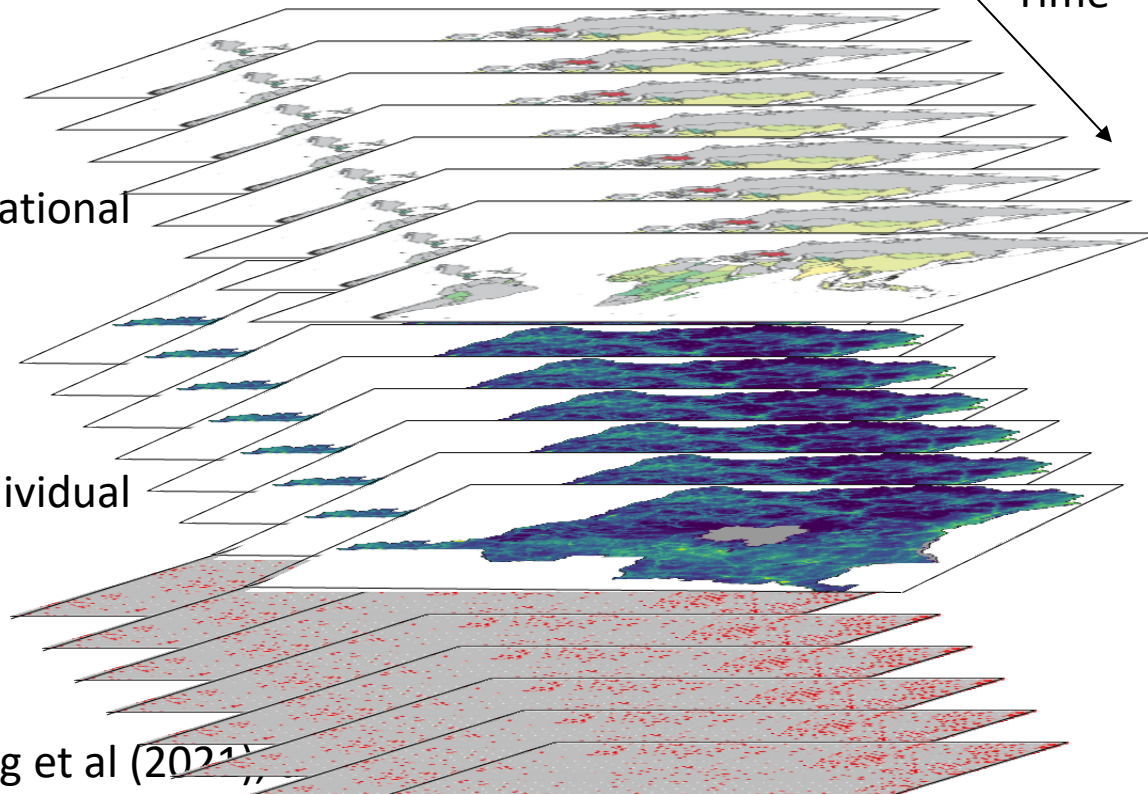
Global, Continental, National

Time

Subnational

Individual

We want to model individual agents on multi-national scales, but space is not the only one...



Figures from Winter et al (2022), Cheng et al (2021),

Related work on importations?

Relative risk of importations by state and month

